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### Authors

Hernandez-Maldonado, Jaime
Stoneburner, Brendon
Boren, Alison
et al.



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# Genome Sequence of the Photoarsenotrophic Bacterium *Ectothiorhodospira* sp. Strain BSL-9, Isolated from a Hypersaline Alkaline Arsenic-Rich Extreme Environment

**Jaime Hernandez-Maldonado,[a] Brendon Stoneburner,[a] Alison Boren,[a] Laurence Miller,[b] Michael Rosen,[c] Ronald S. Oremland,[b] Chad W. Saltikov[a]**

Department of Microbiology and Environmental Toxicology, University of California Santa Cruz, Santa Cruz, California, USA[a]; U.S. Geological Survey, Menlo Park, California, USA[b]; U.S. Geological Survey, Carson City, Nevada, USA[c]

**The full genome sequence of *Ectothiorhodospira* sp. strain BSL-9 is reported here. This purple sulfur bacterium encodes an *arxA*-type arsenite oxidase within the *arxB2AB1CD* gene island and is capable of carrying out "photoarsenotrophy" anoxygenic photosynthetic arsenite oxidation. Its genome is composed of 3.5 Mb and has approximately 63% G+C content.**

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Address correspondence to Chad W. Saltikov, saltikov@ucsc.edu.

Arsenic-rich soda lakes are ideal environments for culturing microorganisms with unique metabolic capabilities for coupling cellular energy production to arsenic oxidation and reduction (1–6). Here, we report the assembled genome of an anoxygenic photosynthetic arsenite-oxidizing ("photoarsenotrophic") bacterium, *Ectothiorhodospira* sp. strain BSL-9. This microbe was isolated from Big Soda Lake, an arsenic-rich (~25 $\mu$M), hypersaline (26 to 88 g/liter total dissolved solids), alkaline (pH 9.7) lake located in Nevada (39°31′N 118°52′W) (7–9). Moreover, this crater lake has a well-defined seasonal bloom of purple sulfur bacteria (*Chromatium* and *Ectothiorhodospira* species) (10) that are proposed to contribute to the arsenic geochemical cycle.

Assessment of the BSL-9 genome revealed an arsenic gene island, *arxB2AB1CD* (11), which is predicted to encode the arsenite oxidase gene *arxA*. Moreover, *arxB2AB1CD* encodes a [4Fe-4S]-containing protein (*arxB2*), a second [4Fe-4S]-containing protein (*arxB1*), a membrane protein (*arxC*), and a TorD-like protein involved in molybdenum enzyme biogenesis (*arxD*). In the chemoautotrophic bacterium *Alkalilimnicola ehrlichii* sp. strain MLHE-1, *arxA* is required for anaerobic arsenite oxidation coupled to nitrate (12). The BSL-9 genome lacks the AioA-type arsenite oxidase. A BSL-9 *arxA* mutant strain shows that *arxA* is the sole arsenite oxidase for photoarsenotrophy (13).

*Ectothiorhodospiraceae* are common anoxygenic phototrophs with versatile abilities to metabolize inorganic and organic electron donors (14–16), which enables them to occupy distinct euphotic hypersaline alkaline environments. In addition to arsenite, BSL-9 can grow photoautotrophically with sulfide or thiosulfate. This is consistent with the presence of *sox* and *dsr* genes, which are involved in sulfur oxidation (17, 18). Moreover, BSL-9 can also grow as a photoheterotroph with various organic acids (e.g., acetate, malate, propionate, lactate, fumarate, succinate, and pyruvate). BSL-9 is sensitive to chloramphenicol, resistant to kanamycin, carbenicillin, gentamicin, and tetracycline, and grows optimally at 35°C at pH 8, 2% NaCl; these growth patterns are consistent with other *Ectothiorhodospira* species (14–16). Although BSL-9 is an anaerobe, the presence of cytochrome *c* oxidase genes (e.g. $cbb_3$) found in BSL-9 may explain its tolerance to atmospheric oxygen. For example, cytochrome *c* oxidases ($cbb_3$) are known for having high oxygen affinity, and cytochrome *c* peroxidases protect cells from reactive oxygen species. The BSL-9 genome also encodes photosynthetic complex genes, such as bacteriochlorophyll *a* synthase, the light-harvesting complex *pucAB*, and two copies of the carbon fixation-related gene *rbcL* (type III RuBisCO). Having the full genome sequence of BSL-9 opens numerous possibilities for studying the metabolic abilities, physiology, and the ecological environmental impact of photoarsenotrophy to the arsenic biogeochemical cycle.

The genome was done at the UC Davis Genome Sequencing Center using PacBio technology. The Hierarchical Genome Assembly Process (HGAP_v2) assembly pipeline (19) was used with ~300× sequence coverage. For annotation, the NCBI Public Genome Annotation Pipeline service was used. The resulting assembly was 3.5 Mb, with 63% G+C content.

**Accession number(s).** The genome sequence of *Ectothiorhodospira* sp. strain BSL-9 was deposited in the GenBank database under the accession no. CP011994, NCBI BioProject accession no. PRJNA232800, and BioSample accession no. SAMN03795182.

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